Freeform Search

10077383

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- Derwent World Patents Index
- IBM Technical Disclosure Bulletins

Term: 13 and RNAseH

Display: 10 **Documents in Display Format:** - **Starting with Number** 1

Generate: ○ Hit List ◉ Hit Count ○ Side by Side ○ Image

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Search History

DATE: Thursday, January 06, 2005 Printable Copy Create Case

Set Name side by side	Query	Hit Count	Set Name result set
DB=USPT,EPAB,JPAB,DWPI; PLUR=YES; OP=ADJ			
L7	l3 and RNAseH	4	L7
L6	l4 and reverse transcriptase$1	0	L6
L5	l3 and (reverse transcriptase$1 near5 (lack$1 or devoid$3) near5 RNaseH)	0	L5
L4	L3 and (reverse transcriptase near5 lack$1 near5 RNaseH)	0	L4
L3	(primer$1 or oligonucleotide$1) same (brideg$3 sequence$1 or spac$3 sequence$1)	239	L3
L2	L1 and (reverse transcriptase$1 near5 lack$1 near5 RNAseH)	1	L2
L1	(primer$1 or oligonucleotide$1)same (brideg$3 or spac$3)	5030	L1

END OF SEARCH HISTORY

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> s (primer# or oligonucleotide#) (P) (brideg### sequence# or spac### sequence#)
L1          291 (PRIMER# OR OLIGONUCLEOTIDE#) (P) (BRIDEG### SEQUENCE# OR SPAC##
                # SEQUENCE#)

=> s l1 and reverse transcriptase#(10a)lack#(10a)RNAseH
L2            0 L1 AND REVERSE TRANSCRIPTASE#(10A) LACK#(10A) RNASEH

=>  s l1 and (reverse transcriptase#(10a)lack#(10a)RNAseH)
L3            0 L1 AND (REVERSE TRANSCRIPTASE#(10A) LACK#(10A) RNASEH)

=> s l1 and reverse transcriptase#
L4            8 L1 AND REVERSE TRANSCRIPTASE#

=> s l4 and RNAseH
L5            1 L4 AND RNASEH

=> d l5 bib ab kwic

L5   ANSWER 1 OF 1  CAPLUS  COPYRIGHT 2005 ACS on STN
AN   2002:946303  CAPLUS
DN   138:1057
TI   Nucleic acid amplification utilizing intermediate duplexes
IN   Haydock, Paul V.; U'Ren, Jack
PA   Saigene Corporation, USA
SO   PCT Int. Appl., 69 pp.
     CODEN: PIXXD2
DT   Patent
LA   English
FAN.CNT 1
     PATENT NO.           KIND   DATE        APPLICATION NO.          DATE
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PI   WO 2002098895         A1    20021212    WO 2002-US18229          20020607
         W:  AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN,
             CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH,
             GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR,
             LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH,
             PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ,
             UA, UG, US, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU,
             TJ, TM
         RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH,
             CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR,
             BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG
     US 2003050444          A1    20030313    US 2002-77383            20020215
     EP 1404697             A1    20040407    EP 2002-737437           20020607
         R:  AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,
             IE, SI, LT, LV, FI, RO, MK, CY, AL, TR
PRAI US 2001-296812P       P     20010607
     US 2002-77383         A     20020215
     WO 2002-US18229       W     20020607
OS   MARPAT 138:1057
AB   This invention provides for a novel amplification procedure for nucleic
     acid.  The method uses a wild type or mutant RNA polymerase designed to
     transcribe both deoxyribonucleotides and ribonucleotides.  The invention
     provides for oligonucleotide primers that comprise in
     the following order from 5' to 3': a phage-encoded RNA polymerase
     recognition sequence, a spacer sequence comprising a
     sequence of from 12 to 20 nucleotides that consists of one nucleotide or
     two different nucleotide types, and a target complimentary sequence which
     can bind a segment of a target nucleic acid.  The target nucleic acid can
     be ssDNA or comprised of RNA.  The invention further provides a kit for
     amplifying a target nucleic acid, containing a wild type or a mutant phage RNA
     polymerase competent to incorporate dNTP and rNTP simultaneously into a
     template nucleic acid.
RE.CNT  1     THERE ARE 1 CITED REFERENCES AVAILABLE FOR THIS RECORD
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ALL CITATIONS AVAILABLE IN THE RE FORMAT

AB This invention provides for a novel amplification procedure for nucleic acid. The method uses a wild type or mutant RNA polymerase designed to transcribe both deoxyribonucleotides and ribonucleotides. The invention provides for **oligonucleotide primers** that comprise in the following order from 5' to 3': a phage-encoded RNA polymerase recognition sequence, a **spacer sequence** comprising a sequence of from 12 to 20 nucleotides that consists of one nucleotide or two different nucleotide types, and a target complimentary sequence which can bind a segment of a target nucleic acid. The target nucleic acid can be ssDNA or comprised of RNA. The invention further provides a kit for amplifying a target nucleic acid, containing a wild type or a mutant phage RNA polymerase competent to incorporate dNTP and rNTP simultaneously into a template nucleic acid.

ST nucleic acid amplification phage RNA polymerase kit **oligonucleotide primer**; intermediate duplex amplification **spacer sequence** dNTP rNTP

IT 9068-38-6, **Reverse transcriptase**
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(**RNaseH**-; nucleic acid amplification utilizing intermediate duplexes)

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=> dup rem l4
PROCESSING COMPLETED FOR L4
L6             3 DUP REM L4  (5 DUPLICATES REMOVED)

=> d l6 1-3 bib ab kwic

L6   ANSWER 1 OF 3  CAPLUS  COPYRIGHT 2005 ACS on STN
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             GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR,
             LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH,
             PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ,
             UA, UG, US, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU,
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IT 9068-38-6, **Reverse transcriptase**
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(RNaseH-; nucleic acid amplification utilizing intermediate duplexes)

L6 ANSWER 2 OF 3 MEDLINE on STN DUPLICATE 1
AN 94118405 MEDLINE
DN PubMed ID: 7507181
TI A specific orientation of RNA secondary structures is required for initiation of reverse transcription.
AU Aiyar A; Ge Z; Leis J
CS Department of Biochemistry, Case Western Reserve University School of Medicine, Cleveland, Ohio 44106.
NC CA38046 (NCI)
P30 CA 43703 (NCI)
SO Journal of virology, (1994 Feb) 68 (2) 611-8.
Journal code: 0113724. ISSN: 0022-538X.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals; AIDS
EM 199402
ED Entered STN: 19940312
Last Updated on STN: 19970203
Entered Medline: 19940218

AB The 5' end of avian retrovirus RNA near the **primer**-binding site (PBS) forms two secondary structures, the U5-inverted repeat (U5-IR) and the U5-leader stems, and contains a 7-nucleotide sequence that anneals to the T psi C loop of the tRNA(Trp) **primer**. Mutations that disrupt any of these base pair interactions cause defects in initiation of reverse transcription both in vivo and in vitro (D. Cobrinik, A. Aiyar, Z. Ge, M. Katzman, H. Huang, and J. Leis, J. Virol. 65:3864-3872, 1991; A. Aiyar, D. Cobrinik, Z. Ge, H.-J. Kung, and J. Leis, J. Virol. 66:2464-2472, 1992). We have now examined the effect of perturbing the non-base-paired intervening "**spacer**" **sequences** between these secondary-structure elements. Small deletions or insertions in these intervening sequences decreased initiation of reverse

transcription in vitro. In contrast, base substitutions, which maintain the spacing distances between the structures, had no detectable effect. Additionally, a small deletion at the 3' end of the PBS caused a significant decrease in initiation of reverse transcription whereas substitution mutations again had no effect. Together, these results indicate that **reverse transcriptase** forms a complex in which the different structural elements are maintained in a specific orientation that is required for efficient initiation of reverse transcription. Specific sequence recognition of the duplex structures by **reverse transcriptase** is also required since mosaic RNAs that combine the human immunodeficiency virus type 1 PBS with avian sequences is not efficiently utilized for reverse transcription even though the **primer** used can anneal to the substituted PBS.

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L6 ANSWER 3 OF 3 CAPLUS COPYRIGHT 2005 ACS on STN DUPLICATE 2
AN 1991:36720 CAPLUS
DN 114:36720
TI Sequence, organization and transcription of the ribosomal RNA operon and the downstream tRNA and protein genes in the archaebacterium Thermofilum pendens
AU Kjems, Joergen; Leffers, Henrik; Olesen, Tina; Holz, Ingelore; Garrett, Roger A.
CS Kem. Inst., Aarhus Univ., Aarhus, 8000, Den.
SO Systematic and Applied Microbiology (1990), 13(2), 117-27
CODEN: SAMIDF; ISSN: 0723-2020
DT Journal
LA English
AB The single rRNA (rRNA) operon from the extremely thermophilic archaebacterium T. pendens was sequenced together with the immediate downstream tRNA genes and open reading frames on both DNA strands. The genes for 16S and 23S RNA were separated by a short **spacer** **sequence** and were not followed by a 5S RNA gene. Sites of initiation and termination of the rRNA transcript, and its processing sites, were localized by S1 or mung bean nuclease mapping and by **primer**-directed **reverse transcriptase** anal. Initiation occurred primarily 187 nucleotides upstream from the 16S RNA gene, after an archaebacterial promoter and this was confirmed by a guanyltransferase capping experiment The transcript terminated inefficiently before a polypyrimidine sequence 45 nucleotides downstream from the 23S RNA gene. The 16S RNA leader sequence, the spacer region and the sequence downstream from the 23S RNA can generate extensive secondary structure, including the processing stems for the 2 rRNAs. Moreover, much of this structure is supported phylogenetically by coordinated base changes. It

is proposed that some of these double helical structures are involved in transcriptional regulation. The 16S and 23S RNA sequences were aligned with those of other organisms. Secondary structures were generated from the alignments which are characteristic of the extreme thermophiles. Moreover, phylogenetic trees were derived which placed T. pendens close to Thermoproteus tenax. The downstream tRNA genes and open reading frames each exhibited an archaebacterial promoter-like motif and a putative primary initiation site. Incomplete termination also occurred at polypyrimidine sequences. A 919-bp sequence between the 2 tRNA genes, which are located on opposing DNA strands, was rich in polypyrimidine sequences on both strands. Transcript mapping suggested that this constitutes a major termination region.

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